

ND

OM of: US-09-784-340-2 to: EST: * out_format : pfs
Date: Aug 27, 2001 7:41 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

-MODEL=frame+g2n.model -DEV=xlp
-O/cgn2.1/USPTO_spool/US09784340/runat_27082001.123146.78/app-query.fasta.1.591
-DB=EST -QFMT=fastap -SUFFIX=olip2n.rst -GAPOP=4.500
-GAPOP=0.050 -MINMATCH=0.100 -LOOPL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
-DELOP=6.000 -XGAPEXT=7.000 -XGAPOP=60.000 -XGAPEXT=60.000
-DELOP=6.000 -DEEXT=7.000 -START=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=quality
-THR_MIN=1 -ALIGN=1 -MODE=LOCAL -OUTEXT=pfs -NORM=ext -MINLEN=0
-MAXLEN=2000000000 -USER=US09784340.ccgcn1.1.3561 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPHY -WAIT -THREADS=1

Search information block:

Query: US-09-784-340-2
Query length: 527
Database: EST: *
Database sequences: 10728115
Database length: 431459454
Search time (sec): 1332.720000

WARN: XGAPOP and XGAPEXT must be equal. Assuming XGAPOP=XGAPEXT=60.000
WARN: XGAPEXT and XGAPEXT must be equal. Assuming XGAPEXT=XGAPEXT=60.000

score_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
gb_est198:BG249053	+	83.00	1302.32	1.5e-74	671
gb_gss8:AO206472	+	74.00	1338.91	1.9e-65	501
gb_gss36:BB0712	+	54.00	971.77	5.2e-45	444
gb_gss10:AO311717	-	44.00	785.45	1.2e-34	601
gb_est18:AI303265	-	41.00	731.62	1.2e-31	501
gb_est25:AI791045	+	41.00	731.26	1.3e-31	525
gb_est24:AI788285	+	41.00	730.47	1.4e-31	583
gb_est16:AI158921	-	41.00	729.46	1.6e-31	666
gb_est21:AI529553	-	41.00	727.74	2.0e-31	836
gb_hic:AA008601	+	41.00	720.76	5.0e-31	2099
gb_est100:BG040124	+	37.00	653.58	2.8e-27	898
gb_est83:BF080415	+	33.00	585.52	1.8e-23	449
gb_est14:AF0202345	+	33.00	584.67	1.9e-23	483
gb_est83:BF080461	+	33.00	583.59	2.2e-23	557
gb_est109:TF7857	+	28.00	494.03	2.1e-18	403
gb_est40:AV655524	+	28.00	493.90	2.2e-18	410
gb_est40:AV655524	+	28.00	493.84	2.2e-18	413
gb_est14:AA962194	-	28.00	493.50	2.3e-18	432
gb_est14:AA967868	-	28.00	492.67	2.5e-18	482
gb_gss10:AO311499	-	28.00	492.18	2.7e-18	514
gb_est20:AI480418	-	28.00	491.95	2.8e-18	730
gb_est91:BF688309	+	28.00	489.36	3.9e-18	746
gb_est40:AV681832	+	28.00	489.16	4.0e-18	766
gb_est25:AI821970	-	26.00	453.38	3.9e-16	669
gb_est20:AI433838	-	25.00	437.00	3.2e-15	512
gb_est83:BF132129	+	25.00	436.63	3.3e-15	538
gb_est13:AA891683	-	24.00	418.87	3.3e-14	494
gb_est13:AA893486	-	24.00	418.84	3.3e-14	496
gb_est14:AA945116	-	24.00	417.82	3.7e-14	568
gb_est53:AW916387	+	24.00	417.29	4.0e-14	609
gb_est100:BG427877	+	24.00	414.04	6.1e-14	935
gb_est40:AV693253	+	23.00	403.64	2.3e-13	325
gb_est44:AM237578	+	23.00	403.28	2.7e-13	341
gb_est109:TF50951	+	23.00	402.38	2.8e-13	384
gb_est3:AA209027	+	23.00	402.15	2.8e-13	395
gb_est61:BB283558	-	23.00	400.15	3.0e-13	515
gb_est22:AI627658	-	23.00	399.98	3.7e-13	527
gb_est20:AI451845	-	23.00	399.78	3.8e-13	541
gb_est65:BE013295	+	23.00	399.60	3.9e-13	554

gb_est18:AI265736 - 23.00 399.59 3.9e-13 555
gb_est18:AI265404 - 23.00 399.52 3.9e-13 550
gb_est19:AI391413 + 23.00 399.40 4.0e-13 559
gb_est86:BF322562 - 23.00 398.52 4.4e-13 539
gb_est43:AW129268 - 22.00 382.94 3.3e-12 410
gb_gss15:AO728754 - 22.00 382.38 3.5e-12 474

seq_name: gb_est98:BG249053

seq_documentation_block: 671 bp mRNA 13-FEB-2001

LOCUS BG249053 602361828P1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4470199 5'

DEFINITION mRNA sequence.

ACCESSION BG249053 GI:12758869

VERSION EST.

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 671)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapds@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: LLM10287 row: h column: 08

High quality sequence stop: 661.

Location/Qualifiers

1..671

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4470199"

/clone.lib="NIH_MGC_89"

/tissue_type="hypertrophied, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: Kidney; Vector: pCMV-Sport6; Site: 1: Not; Site: 2: Salt; Cloned unidirectionally; oligo-dT primed. Average insert size 1.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC library."

BASE COUNT 206 a 123 c 153 g 189 t

ORIGIN

alignment_scores:

Quality: 83.00 Length: 83

Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-784-340-2 x BG249053

Align seg 1/1 to: BG249053 from: 1 to: 671

91 ValAspleuAlalaAsnValleupProglyLeuSerThrTrpInserva 107

111 GTTACCTAGCTGGAAGTCTTCCAGGCTTATCAACCTGCAATACGT 160

107 IILtysLeuAsnspPheValGluIleArgGlyThrLeuLysMetM 124

161 TATTAATTAATGATTTTGTGTAATTAAGAGAACTTAATAATGA 210

124 etCysGluSerPheIleTyraSngInThrLeuMetLysLysLeuGln 140

211 TGTGTGAGAGCTTATCTACCAATGAGAGCGCTTATGAGAAGACCTACAGGA 260

141 ThrAsnTyrAspValMetLeuIleAspProValIleProCysGlyAspLe 157
|||||
261 ACCAACTACATGTATGCTTATAGACCTGTGATTCCTGTGGAACCT 310
157 uNcctAlaGluLeuAlaValProPheValLeuThrLeuArgIleSer 173
|||||
311 GATGCTGAGTGTGCTGACATCCCTTTGTGTGCACACTTAGAATTTC 359

seq_name: gb_gss8:AQ206472

seq_documentation_block:
LOCUS AQ206472 501 bp DNA GSS 17-SEP-1998
DEFINITION HS_3241_A2_G09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 COL=18 Row=M, DNA sequence.
ACCESSION AQ206472
VERSION AQ206472.1 GI:3617042
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 501)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3241 Row: M Column: 18
Class: BAC ends
High quality sequence stop: 501.
Location/Qualifiers
1..501
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 135 a 110 c 93 g 160 t 3 others

ORIGIN

alignment_scores:
Quality: 74.00 Length: 74
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-784-340-2 x AQ206472 ..

Align seg 1/1 to: AQ206472 from: 1 to: 501

454 ProLeuAspArgAlaValPheTrpIleGluPheValMetArgHisIysG1 470
|||||
46 CCCCTAGATCGACACGCTTCTGATCGAGTTGTGTCATGCGCCACAAGG 95
470 yAlaLysHisLeuArgSerAlaAlaHisAspLeuThrTrpPheGlnHisT 487
|||||
96 AGCGAAGCACCTGCGATCAGCTGCCATGACCTGCACCTGCTTCACACACT 145
487 ySerIleAspValIleGlyPheLeuLeuThrcysValAlaThrAlaIle 503

146 ACTCTATAGATGATGGATTGCTCTGACCTGTGTGCACTGTATA 195
|||||
504 PheLeuPheThrLysCysPheLeuPheSerCysGlnLysPheAsnLysTh 520
|||||
196 TCTCTGTTACAAAGATGTTTATTATTTCTGTCAAAAATTAATAAAG 245
520 rArgLysIleGluLysArgGlu 527
|||||
246 TAGAAAGATAGAAAGAGCGAA 267

seq_name: gb_gss36:B80712

seq_documentation_block:
LOCUS B80712 444 bp DNA GSS 24-OCT-1998
DEFINITION CIT-HSP-2050M23.TF CIT-HSP Homo sapiens genomic clone 2050M23, DNA sequence.
ACCESSION B80712
VERSION B80712.1 GI:2867735
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 444)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M., and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
Unpublished (1998)
JOURNAL other_GSSs: CIT-HSP-2050M23.TR
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html
Seq primer: MJ3-21
Class: BAC ends.
Location/Qualifiers
1..444
/organism="Homo sapiens"
/db_xref="GDB:7056698"
/db_xref="taxon:9606"
/clone_lib="2050M23"
/clone_lib="CIT-HSP"
/sex="male"
/cell_type="Sperm"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"

BASE COUNT 124 a 110 c 71 g 139 t

ORIGIN

alignment_scores:
Quality: 54.00 Length: 54
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-784-340-2 x B80712 ..

Align seg 1/1 to: B80712 from: 1 to: 444

434 SerSerTyrLysGluAsnAlaMetArgLeuSerArgIleHisAspG1 450
|||||
282 TCCAGTTATTAAGAGCAATCTATGAGATTATCAAGATTTCACCATGATCA 331


```

    /sex="female"  

    /dev string="adult"  

    /lab_host="DH10B"  

    /note-Organ: Kidney; Vector: pMEI8S-FL3; Site_1: DraIII  

    (/CAGGTG); Site_2: DraIII (CACCATGG); 1st strand cDNA  

    was primed with an oligo(dT) primer  

    [ATCGGCCCTTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was  

    ligated to a DraIII adaptor [TGTCGCCTACTACGG], digested  

    and cloned into distinct DraIII sites of the pMEI8S-FL3  

    vector (' site CACTGTGG, 3' site CACCATTG). XhoI should  

    be used to isolate the cDNA insert. Size selection was  

    performed to exclude fragments <1.5kb. Library  

    constructed by Dr. Sumio Sugano (University of Tokyo  

    Institute of Medical Science). Custom primers for  

    sequencing: 5' end primer CTYTCGCTTTAAAGCTGCG and 3' end  

    primer CGACCTCCAGCTCGACACA."

```

BASE COUNT 146 A 130 C 154 G 152 T 1 others

ORIGIN

Alignment scores:

	Quality:	Ratio:	Percent Similarity:	Length:	Gaps:	Percent Identity:
	41.00	1.000	100.000	41	0	100.000

alignment_block:
US-09-784-340-2 x AT788285 ..

Align seg 1/1 to: AT788285 from: 1 to: 583

seq_name= gb_estt16:AII158921

Seq_documentation_block:

LOCUS	AII158921	666 bp	mRNA	EST	02-OCT-1998
DEFINITION	Uf05c02.X1 Sugano mouse liver mla Mus musculus cDNA clone IMAGE:1499714 3'				similar to gb:U06641 UDP-GLYCOXYMETHYLTRANSFERASE 2B8 PRECURSOR, MICROSMAL (HUMAN); gb:X06358 Mouse mRNA for UDP-glycoxymethyltransferase (MOUSE):: mRNA sequence.
ACCESSION	AII158921				
VERSION	AII158921.1	GI:3692103			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 666)				
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubouque,T., Schellenberg,K., Steptoe,W., Tan,F., Underwood,K., Moore,B., Theising,R., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.				
TITLE	The Mashu-HMI Mouse EST Project				
JOURNAL	Unpublished (1996)				
COMMENT	Contact: Marra M/Mouse EST Project Washu-HMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: mousetest@wustl.edu This clone is available royalty-free through LIND ; contact the				

IMAGE Consortium (infoimage.llnl.gov) for further information.
MGI:937338
Seq primer: custom primer used
High quality sequence stop: 464.
Location/Qualifiers

1. .666
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:149714"
/clone_id="Sugano mouse liver: mlia"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: liver; Vector: pMEI8S-FL3; Site_1: DraIII (CACGTGtg); Site_2: DraIII (ACCATGtg); 1st strand cDNA was primed with an oligo(dT) primer [ATGGGCCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated into distinct DraIII sites of the pMEI8S-FL3 vector (5' site CACTGTg, 3' site CACCAgtg). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGCTCTAAGAGTGCG and 3' end primer CGACCTGCACGCTGACACA."

BASE COUNT 178 a 144 c 139 g 203 t 2 others
ORIGIN

alignment_scores:
Quality: 41.00 Length: 41
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-784-340-2 x AII58921/rev ..
Align seg 1/1 to reverse of: AII58921 from: 1 to: 666

seq_name: gb_est21:A1529553

seq_documentation_block:
LOCUS A1529553 836 bp mRNA EST 18-MAR-1999
DEFINITION u182a02.x1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1888874.3 similar to gb:U06641 UDP-Glucuronosyltransferase
2B8 PRECURSOR, MICROSMAL (HUMAN); gb:X06358 mouse mRNA for
UDP-glucuronosyltransferase (MOUSE); mRNA sequence.

ACCESSION A1529553
VERSION A1529553.1 GI:443688
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 836)
Matta,M., Hillier,L., Kueba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers,Y., Peterson,
B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Riltter
, E., Kohm,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,

ELGARGHEVTLVKPSIITIDSKRIPIPHENIPILEYEITAEENRLNIANLVNIPN
 ISIMBAKTIODEPFIQVOTGDEFSICRSVYXNOKEMKILDAQYDVYVIDPVCCETLV
 AEVLQIPVYTLRFSGMYMEKHGOLPIPLSTVPMVSELDONMFTTRKXMMFSL
 LFEWLMQYDFAFMOQYSETLGRPTTCKTGEADWLIRYWDVEFPRLPINPEF
 VGLGCKRPKPLPKEMEERFVOSGSEGVVFSIGSVKMLTEKANLIASVLAQIPQK
 VLMRSGKKPALIGSNTLRFLNIPONDILGHRTKAFITGGNGIYEALYGVPMWG
 VPMIDOPNINAHMAKGAALKVSISTMTSTPLLSVRVAINPSPYKEMAMRLSRFHH
 DQPVKFLBRAVRIEIEFVHRKAKHLRVAHAHLSMFOYHSLDVIIGLILCVTLITFI
 TRFCEVCKIYMKESKMKMNRKKK"

BASE COUNT 618 a 406 c 467 g 608 t

ORIGIN

alignment_scores: Quality: 41.00 Length: 41
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x AK008601 ..

Align seg 1/1 to: AK008601 from: 1 to: 2099

435 SerTyrIySGIuAsnAlaMetarGleuSerArgIleHisSaspGlnPr 451
 |||||||
 1323 TCTATATAAGAGATGCCATCGGTTATCAAGAAATCCACATGATCAGCC 1372
 451 oValIySProLeuAspArgAlaValaPheTrpIleGluPheValaMetArgH 468
 |||||||
 1373 AGTGAACCCCTGGACAGACAGCGTCTTGATGAGTTTGATCAGCGTC 1422
 468 IStySGIAlaIySHisLeuArg 475
 |||||||
 1423 ACAAGAGACCAACACATCTTCT 1445

seq_name: gb_est100:BG402144

seq_documentation_block:

LOCUS BG402144 898 bp mRNA EST 12-MAR-2001
 DEFINITION 602465689F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4593694 5',
 mRNA sequence.

ACCESSION BG402144
 VERSION BG402144.1 GI:13295592

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 898)
 NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 plate: LICM134 row: a column: 23
 High quality sequence stop: 557.

FEATURES
 source location/Qualifiers

1..898
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4593694"
 /clone_lib="NIH_MGC_75"
 /lab_host="DH10B (r1 phage-resistant)"
 /note="Organ: Kidney; Vector: pDNK-LIB (Clontech); Site: 1:
 SfiI (ggcgctcgcc); Site 2: SfiI (ggccatcagcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor

sequence: 5'-CACGGCATTATGCCC-3' and 3' adaptor sequence:
 5'-ATCTAGAGGCGGAGCGCGCCGACAG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.65
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH-MGC Library."

BASE COUNT 249 a 175 c 165 g 309 t

ORIGIN

alignment_scores: Quality: 37.00 Length: 37
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x BG402144 ..

Align seg 1/1 to: BG402144 from: 1 to: 898

491 ValIleGlyPheLeuLeuThrCysValAlaThrAlaIlePheLeuPheTh 507
 |||||||
 1 GTGATTGGGTTCTCTGCTGACCTGTGTGCGCACTGCTATATCTTTTCAC 50
 507 rLyScySPheLeuPheSerCysGlnIySPheAsnIySThrArgIySileG 524
 |||||||
 51 AAAAGTTTATTATTTTCTCTGTCGCAAAATTTAATTAACCTGAAGATVAG 100
 524 IuLySArgGlu 527
 |||||||
 101 AAAAGAGCGAA 111

seq_name: gb_est83:BF080415

seq_documentation_block:

LOCUS BF080415 449 bp mRNA EST 18-OCT-2000
 DEFINITION 231292 MARC 2Pig Sus scrofa cDNA 5', mRNA sequence.

ACCESSION BF080415
 VERSION BF080415.1 GI:10874245

KEYWORDS EST.

SOURCE pig.

ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 449)
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

AUTHORS Fahnenkrug, S.C., Freking, B.A., Rohrer, J.A., Smith, T.P.L., Casas, E.,
 Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
 and Keeler, J.W.

JOURNAL Design and use of two pooled tissue normalized cDNA libraries for
 EST discovery in swine

COMMENT Unpublished (2000)
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390

Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt. trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -mismatch 12 options.

PCR primers
 FORWARD: AGGAAACAGCTATGACCAT
 BACKWARD: GTTTCGCCAGTCACGACG
 plate: 52 row: O column: 11
 Seq primer: ATTTCAGTGCACACTATAG.

FEATURES
 source location/Qualifiers

1..449
 /organism="Sus scrofa"
 /db_xref="taxon:9823"
 /clone_lib="MARC 2Pig"
 /tissue_type="pooled"
 /lab_host="DH10B"

/note="Vector: PCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT 105 a 116 c 108 g 120 t
ORIGIN

alignment_scores:
Quality: 33.00 Length: 33
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-784-340-2 x BF080415

Align seg 1/1 to: BF080415 from: 1 to: 449

443 LeuserAgtlIleHshisAspgInProValysProLeuAspArgAlaVala 459
|||||
249 TTATCAAGAAATTCACACGATCAACCTGTGAAGCCCTGAGCGGCGGT 298
|||||
459 lPheTPIleGluPheValMetArgHshisGlyAlaValysHshisLeuArg 475
|||||
299 CTCTGGATTGAGTTGTGATGCGCCACAAAGAGCCACGACCTGCGG 347

seq_name: gb_est14:AF202345

seq_documentation_block:

LOCUS AF202345 483 bp mRNA EST 01-NOV-2000
DEFINITION AF202345 Homo sapiens HepG2 Homo sapiens cDNA clone 128-7, mRNA
sequence.

ACCESSION AF202345
VERSION AF202345.1 GI:11068678

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 483)

AUTHORS Horn Davies, C.E., Davis, R.M. and Reidhaar-Olson, J.F.
TITLE Identification of toxicant-induced gene expression changes in HepG2
cells by differential display-PCR
JOURNAL Unpublished (2000)
COMMENT Contact: Horn Davies CE
Affymax Research Institute
3410 Central Expressway, Santa Clara, CA 95051, USA
Email: caroline.davies@affymax.com.

FEATURES
location/Qualifiers
1..483
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="128-7"
/clone_lib="Homo sapiens HepG2"
/cell_line="HepG2"

BASE COUNT 145 a 99 c 104 g 135 t
ORIGIN

alignment_scores:
Quality: 33.00 Length: 33
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-784-340-2 x AF202345

Align seg 1/1 to: AF202345 from: 1 to: 483

443 LeuserAgtlIleHshisAspgInProValysProLeuAspArgAlaVala 459
|||||
104 TTATCAAGAAATTCATCATCAACGATCAACGCGCTGATGATGACGACG 153
|||||
459 lPheTPIleGluPheValMetArgHshisGlyAlaValysHshisLeuArg 475

|||||
154 CTCTGGATTGAGTTGTGATGCGCCACAAAGAGCCACGACCTTCCG 202
seq_name: gb_est83:BF080461

seq_documentation_block:
LOCUS BF080461 557 bp mRNA EST 18-OCT-2000
DEFINITION 231360 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BF080461
VERSION BF080461.1 GI:10874291

KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 557)

AUTHORS Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heston, M.P., Crosse, W.M., Bennett, G.A., Laegreid, W.W.
and Keefe, J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross-match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: ACGAAGACGATGACCAT
BACKWARD: GTTTCCTCCATGACGACG
Plate: 52 row: K column: 13
Seq primer: ATTAGTGACACTATAG.
location/Qualifiers
1..557
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2P1G"
/issue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

FEATURES
source

BASE COUNT 137 a 128 c 138 g 154 t
ORIGIN

alignment_scores:
Quality: 33.00 Length: 33
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-784-340-2 x BF080461

Align seg 1/1 to: BF080461 from: 1 to: 557

443 LeuserAgtlIleHshisAspgInProValysProLeuAspArgAlaVala 459
|||||
251 TTATCAAGAAATTCACACGATCAACCTGTGAAGCCCTGAGCGGCGGT 300
|||||
459 lPheTPIleGluPheValMetArgHshisGlyAlaValysHshisLeuArg 475
|||||
301 CTCTGGATTGAGTTGTGATGCGCCACAAAGAGCCACGACCTGCGG 349

seq_name: gb_est109:T67857

seq_documentation_block:

LOCUS T67857 403 bp mRNA EST 22-FEB-1995
DEFINITION yc27h03.r1 Stratiogene liver (#937224) Homo sapiens cDNA clone

IMAGE:81941 5' similar to gb:J05428 UDP-GLUCURONOSYLTRANSFERASE 2B7
 PRECURSOR, MICROSOMAL (HUMAN); mRNA sequence.

ACCESSION
 VERSION T67857
 KEYWORDS T67857.1 GI:679005

SOURCE
 ORGANISM human.

REFERENCE
 AUTHORS Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 403)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M. F., Chapell, B.,
 Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Le, N., Mardis, E., Moore,
 B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M. B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)

TITLE
 JOURNAL
 MEDLINE

COMMENT
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu

Insert Size: 502

High quality sequence stops: 309 Source: IMAGE Consortium, LNL. This
 clone is available royalty-free through LNL; contact the IMAGE
 Consortium (info@image.llnl.gov) for further information.

Insert Length: 502 Std Error: 0.00
 Seq primer: M13RP1
 High quality sequence stop: 309.

FEATURES
 SOURCE Location/Qualifiers

1. 403
 /organism="Homo sapiens"
 /db_xref="GDB:498998"
 /db_xref="taxon:9606"
 /clone="IMAGE:81941"
 /clone.lib="Stratagene Liver (#937224)"
 /sex="male"
 /dev_stage="49 years old"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: liver; Vector: pBluescript SK; Site: 1: EcoRI
 ; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
 dT. Hepatectomy from normal male caucasian. Average insert
 size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5'
 GAATTCGGCAGAG 3' -3' adaptor sequence: 5'
 CTCGAGTTTTTTTTTTTTTTT 3' t
 BASE COUNT 114 a 72 c 94 g 123 t
 ORIGIN

alignment_scores:
 Quality: 28.00 Length: 28
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x T67857 ..

Align seg 1/1 to: T67857 from: 1 to: 403

448 HtASpGlnProValLysProLeuAspArgAlaValPheTrpIleGluPn 464
 |||||||
 58 CATGATCAACAGTGAAGCCCTGAGTCGAGCAGATCTTGTGATGAATT 107
 |||||||
 464 eValMeArgHtLysGlyValAlaLysHtLysuArg 475
 |||||||
 108 TGTCAATCGCCACAAAGAGACTAAACACCTTCG 141

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